

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 2, 2006, 21:41:17 ; Search time 80 Seconds
(without alignments)
49.430 Million cell updates/sec

Title: US-10-623-176a-2

Perfect score: 45

Sequence: 1 VLHDDLLEA 9

Scoring table: BLOSUM62

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_21:.*
1: geneseqp1980s:.*
2: geneseqp1990s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*
9: geneseqp2005s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	9	2	AAW9196 Minor his
2	45	100.0	9	2	AAW97375 HA-1 H-al
3	45	100.0	9	8	ADH40333 Human min
4	45	100.0	13	2	AAW9199 VR cell K
5	45	100.0	13	2	AAW97415 KIAA0223
6	45	100.0	1165	8	ADSI1768 Human the
7	38	84.4	199	7	ADP06880 Bacterial
8	37	82.2	9	2	AAW9197 Minor his
9	37	82.2	9	2	AAW97374 HA-1 R-al
10	37	82.2	9	8	ADH40334 Human min
11	37	82.2	13	2	AAW9198 DH cell K
12	37	82.2	13	2	AAW97414 KIAA0223
13	37	82.2	1136	5	AD117193 Human NOV
14	37	82.2	1136	5	AD116744 Human NOV
15	37	82.2	1136	8	ADH61299 INTSIG PR
16	37	82.2	1136	8	ADN42398 Human nov
17	37	82.2	1136	8	ADN42398 Human nov
18	37	82.2	1165	5	AD117194 Human NOV
19	37	82.2	1165	8	ADP55035 Human PRO
20	37	82.2	1165	8	ADP24600 PRO polyP
21	36	80.0	9	2	AAW9195 Minor his
22	35	77.8	148	8	ADG5728 T-cell ep
23	35	77.8	148	8	ADG5728 Novel hum
24	35	77.8	496	6	ABM71411 Staphyloc

25	35	77.8	608	7	ABO77464	ABO77464 Pseudomon
26	35	77.8	786	6	ABU29875	Abu29875 Protein e
27	35	77.8	786	9	ADV16669	Adv16669 E. faeciu
28	35	77.8	789	7	ADG97107	Adg97107 E. faeciu
29	35	77.8	964	7	ADB70281	Abd70281 C. neofo
30	35	77.8	130	6	ABU26589	Abu26589 Protein e
31	34	75.6	130	9	AEA22128	Aea22128 Campyloba
32	34	75.6	232	4	ABM55593	Abm55593 Propionib
33	34	75.6	232	6	ABM52112	Abm52112 Propionib
34	34	75.6	253	6	ABU42064	Abu42064 Protein e
35	34	75.6	332	4	ABB64157	Abb64157 Drosophil
36	34	75.6	385	6	ABU41832	Abu41832 Protein e
37	34	75.6	440	4	AA874623	Aa874623 Saitocella
38	34	75.6	446	6	ABU34950	Abu34950 Protein e
39	34	75.6	554	8	ADY09404	Ady09404 Plant ful
40	34	75.6	680	8	ADY48425	Ady48425 Maize oil
41	34	75.6	774	4	ABB65640	Abb65640 Drosophil
42	34	75.6	774	4	AU38963	Aau38963 Drosophil
43	34	75.6	774	7	ADC35871	Adc35871 Drosophil
44	34	75.6	783	4	AG91263	Aag91263 C glutam
45	34	75.6	802	7	AA838199	Aa838199 Fruit fly

ALIGNMENTS

RESULT 1
AAW9196 standard; peptide; 9 AA.
XX
XX
AC
XX
AAW9196;
XX

20-MAY-1999 (first entry)

Minor histocompatibility antigen HA-1 T-cell epitope #2.

Minor histocompatibility antigen; HA-1; T-cell epitope; immunological; graft versus host disease; bone marrow transplant; leukaemia; vaccine; diagnosis; aplastic anaemia; immune deficiency disease.

OS Homo sapiens.

PN WO9905174-A1.

PD 04-FEB-1999.

PF 23-JUL-1998; 98WO-NL000425.

PR 23-JUL-1997; 97EP-00202303.

(UYLE-) RICKSUNITV LEIDEN.

Goulmy EAJM, Hunt DF, Engelhard VH;

WPL; 1999-15312/13.

A new minor histocompatibility antigen, HA-1 - useful to treat immune diseases and prevent rejection and host versus graft disease in bone marrow and organ transplantation.

Claim 3; Page 32; 47pp; English.

The present sequence represents a new peptide (PI) constituting a T-cell epitope obtainable from the minor histocompatibility antigen HA-1. The peptide is immunogenic and can be used as part of a vaccine. PI is used as a medicine, to induce tolerance for transplants, prevent rejection and/or graft versus host disease, or to treat (auto) immune diseases. In particular it can be used with bone marrow transplantation, in the treatment of severe aplastic anaemia, leukaemia, and immune deficiency diseases

Sequence 9 AA;

Query Match 100.0%; Score 45; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHDDLLEA 9
 |||||
 Db 1 VLHDDLLEA 9

RESULT 2
 AAW97375

AAW97375 standard; protein; 9 AA.

AC AAW97375;

DT 13-MAY-1999 (first entry)

DE HA-1 H-allele sequence.

XX Intron; minor histocompatibility antigen HA-1; typing allele; H allele;
 KW R allele; polymorphic nucleotide; HA-1 typing; bone marrow transplant;
 KW severe aplastic anaemia; leukaemia; immune deficiency disease; ss.

OS Homo sapiens.

PN WO9905313-A2.

PD 04-FEB-1999.

PF 23-JUL-1998; 98WO-EP004928.

PR 23-JUL-1997; 97EP-00202303.

PR 02-JUN-1998; 98EP-00870125.

PA (UYLE-) RIJCKSUNIV LEIDEN.

PI Goulmy E;

DR WPI, 1999-142960/12.

PT Typing minor histocompatibility antigen HA-1 - by amplifying and
 identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection
 of genetic aberrances.

PS Claim 18, Fig 5, 59pp; English.

XX The present sequence represents part of the minor histocompatibility
 CC antigen HA-1 H-allele. The specification describes methods for typing
 CC alleles (preferably the H and R alleles) of the minor histocompatibility
 CC antigen HA-1 in a sample, which comprise detecting polymorphic
 CC nucleotides in the cDNA or genomic nucleic acids of the alleles. The
 CC methods can be used for HA-1 typing for bone marrow transplants, severe
 CC aplastic anaemia, leukaemia and immune deficiency diseases, as well as
 CC detection of genetic aberrances. The probes and primers of the invention
 CC can be used to screen for the HA-1 alleles. The HA-1 peptides can be used
 CC anti-idiotypic B cells and/or T cells and antibodies

SQ Sequence 9 AA;

Query Match 100.0%; Score 45; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHDDLLEA 9
 |||||
 Db 1 VLHDDLLEA 9

RESULT 3
 ADH40333

ID ADH40333 standard; peptide; 9 AA.

XX ADH40333;
 AC

XX 11-MAR-2004 (first entry)

DT Human minor histocompatibility antigen HA-1 T cell epitope.

DE human; cytostatic; vaccine; SNP profile; cancer; leukaemia;

KW minor histocompatibility antigen; mRNA; T cell epitope.

OS Homo sapiens.

PN WO2003106692-A2.

PD 24-DEC-2003.

PF 13-JUN-2003; 2003WO-EP006251.

PR 13-JUN-2002; 2002EP-00013423.

PA (MERE) MERCK PATENT GMBH.

PI Strittmatter W, Moll H;

DR WPI; 2004-082200/08.

PT Providing allelic variant epitope of protein based on single nucleotide
 polymorphism by defining target protein, screening database of protein,
 identifying, selecting allelic variant protein, creating variant
 epitopes.

PS Disclosure; Page 82; 119pp; English.

XX The invention relates to a novel method for providing epitopes of allelic
 CC variants of antigenic proteins from specific species based on single
 CC nucleotide polymorphism (SNP), by defining target protein/peptide or its
 CC subunit, screening database of DNA encoding target protein, identifying,
 CC selecting allelic peptide/protein variants, expression product or its
 CC fragment encoded by DNA sequence having SNP, creating variant epitopes,
 CC selecting epitopes binding to MHC protein. A protein of the invention has
 CC cytostatic activity, and may have a use in a vaccine. The method is
 CC useful for generating a SNP profile of one or more individuals from a
 CC given species by applying the method for several protein from the
 CC individuals, where the SNP profile was related to disease, preferably
 CC cancer. This is useful for diagnosing a disease in an individual by
 CC generating the SNP-related polymorphic profile. A method of the invention
 CC is useful for transplanting haematopoietic stem cells from a donor to a
 CC recipient and treating cancer, preferably leukaemia, and for determining
 CC the progression, regression or onset of a treated disease. The present
 CC sequence is used in the exemplification of the invention.

SQ Sequence 9 AA;

Query Match 100.0%; Score 45; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHDDLLEA 9
 |||||
 Db 1 VLHDDLLEA 9

RESULT 4
 AAW99199

ID AAW99199 standard; peptide; 13 AA.

AC AAW99199;

DT 20-MAY-1999 (first entry)

DE VR cell K1A0223 protein sequence.

XX Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
 KW graft versus host disease; bone marrow transplant; leukaemia; vaccine;
 diagnosis; aplastic anaemia; immune deficiency disease.

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OM protein - protein search, using sw model

Run on: March 2, 2006, 21:41:50 ; Search time 16 Seconds
(without alignments)
54.122 Million cell updates/sec

Title: US-10-623-176A-2

Perfect score: 45
Sequence: 1 VLHDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	84.4	1148	2	S51855
2	37	82.2	1165	2	D59433
3	35	77.8	119	2	T00151
4	35	77.8	604	2	S36487
5	35	77.8	605	2	S36469
6	35	77.8	616	2	C69226
7	34	75.6	130	2	A81316
8	33	73.3	145	2	A41652
9	33	73.3	174	2	C89075
10	33	73.3	210	2	T44122
11	33	73.3	210	2	B89762
12	33	73.3	238	2	S76860
13	33	73.3	249	2	AC0461
14	33	73.3	259	2	D83601
15	33	73.3	291	2	D83371
16	33	73.3	320	2	B75457
17	33	73.3	322	2	C83075
18	33	73.3	343	2	A10581
19	33	73.3	343	2	B85564
20	33	73.3	343	2	F90713
21	33	73.3	343	2	A45251
22	33	73.3	378	2	T35403
23	33	73.3	397	2	S09813
24	33	73.3	398	2	H72660
25	33	73.3	519	1	S69988
26	33	73.3	519	1	S69989
27	33	73.3	604	2	S36493
28	33	73.3	654	2	AH0668
29	33	73.3	667	2	G90883

30	33	73.3	667	2	H85734	probable collagena
31	33	73.3	667	2	F64895	hypothetical prote
32	33	73.3	723	2	F85047	hypothetical prote
33	33	73.3	856	2	C85023	hypothetical prote
34	33	73.3	908	2	T50695	seca protein (impo
35	33	73.3	973	2	T50449	DNA repair and rec
36	33	73.3	1127	2	S47445	MDM1 protein - yea
37	33	73.3	1770	2	S56221	hypothetical prote
38	33	71.1	91	1	C69973	ribonuclease inhib
39	32	71.1	107	1	R6RM1C	acidic ribosomal p
40	32	71.1	166	2	A42524	A-ORF-E protein -
41	32	71.1	270	2	G84226	hypothetical prote
42	32	71.1	276	2	T28746	hypothetical prote
43	32	71.1	284	2	G70732	probable thiosulfa
44	32	71.1	296	2	T27768	hypothetical prote
45	32	71.1	297	2	A84759	probable trans-pre

ALIGNMENTS

RESULT 1
S51855
hypothetical protein YDR128w - yeast (Saccharomyces cerevisiae)
N/Alternate names: hypothetical protein YD9302.03
C/Species: Saccharomyces cerevisiae
C/Date: 05-May-1995 #sequence_revision 21-Jul-1995 #text_change 05-Oct-2004
C/Accession: S51855
R/Oliver, K.; Harris, D.
Submitted to the EMBL Data Library, February 1995
A/Reference number: S51853
A/Accession: S51855
A/Molecule type: DNA
A/Residues: 1-1148 <ORF>
A/Cross-references: UNIPROT:003897; UNIPARC:UP100006A370; EMBL:Z48179; NID:9665657; PIR
C/Genetics:
A/Genes: MIPS:YDR128w
A/Cross-references: SGD:S0002535
A/Map position: 4R

Query Match
Best Local Similarity 66.7%; Pred. No. 52;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Cy 1 VLHDDLLEA 9
Db 1001 VLHDDLLEA 1009

RESULT 2
D59433
C. elegans protein Z37093 homolog [imported] - human
C/Species: Homo sapiens (man)
C/Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #text_change 09-Jul-2004
C/Accession: D59433; B59433
R/Nagase, T.; Seki, N.; Ishikawa, K.; Ohira, M.; Kawarabayashi, Y.; Ohara, O.; Tanaka, A.
DNA Res. 3, 321-329, 1996
A/Title: Prediction of the coding sequences of unidentified human genes. VI. The coding
A/Reference number: D59433; MUID:97191544; PMID:9039502
A/Accession: D59433
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-1165 <NAG>
A/Cross-references: UNIPROT:092619; UNIPARC:UP10000073EAF; GB:BAI13212; PID:g1504026; PI
R/Ohara, O.; Nagase, T.; Kikuno, R.; Nomura, N.
Submitted to GenBank, August 1996
A/Reference number: B59433
A/Accession: B59433
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1165 <SN02>
A/Cross-references: UNIPARC:UP10000073EAF; GB:BAI13212; PID:g1504026; PIDN:BAI13212.1

Query Match 82.2%; Score 37; DB 2; Length 1165;
 A:Residues: 1-605 <DELA>
 Best Local Similarity 88.9%; Pred. No. 82;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHDDLEA 9
 DB 166 VLHDDLEA 174

RESULT 3

hypotheetical protein 18 - Staphylococcus aureus phage phi PVL

C:Species: Staphylococcus aureus phage phi PVL
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C:Accession: T00151

R:Kaneko, T.; Kimura, T.; Kawakami, Y.; Tomita, T.; Kamio, Y.
 Biosect. Biotechnol. Biochem. 61, 1960-1962, 1997

A:Title: Panton-Valentine leukocidin genes in a phage-like particle isolated from mitomy
 A:Reference number: Z14119; PMID:98067870; PMID:3404084

A:Accession: T00151
 A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 1-119 <KAN>

A:Cross-references: UNIPROT:080057; UNIPARC:UPI000009AFCD; EMBL:AB09866; NID:93341907;
 C:Superfamily: Staphylococcus aureus phage phi PVL hypotheetical protein 18

Query Match 77.8%; Score 35; DB 2; Length 119;
 Best Local Similarity 85.7%; Pred. No. 15;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HDDDLEA 9
 DB 72 HDDDLEA 78

RESULT 4

hypotheetical protein 19 - human papillomavirus type 19

C:Species: human papillomavirus type 19
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 C:Accession: S36487

R:Delius, H.; Hofmann, B.
 submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.
 A:Reference number: S36469

A:Accession: S36487
 A:Molecule type: DNA

A:Residues: 1-604
 A:Cross-references: UNIPROT:Q02048; UNIPARC:UPI00001382F0; EMBL:X74470; NID:9336940; PID
 C:Superfamily: papillomavirus E1 protein

C:Keywords: early protein; nucleus

Query Match 77.8%; Score 35; DB 2; Length 604;
 Best Local Similarity 75.0%; Pred. No. 94;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LHDDLEA 9
 DB 201 VHDDLES 208

RESULT 5

E1 protein - human papillomavirus type 14D

C:Species: human papillomavirus type 14D
 C:Date: 09-Dec-1993 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 C:Accession: S36469

R:Delius, H.; Hofmann, B.
 submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.
 A:Reference number: S36469

A:Accession: S36469

A:Molecule type: DNA
 A:Residues: 1-605 <DELA>
 A:Cross-references: UNIPROT:P36721; UNIPARC:UPI00001382EC; EMBL:X74467; NID:9336918; PID
 A:Experimental source: strain 14D
 C:Superfamily: papillomavirus E1 protein
 C:Keywords: early protein; nucleus

Query Match 77.8%; Score 35; DB 2; Length 605;
 Best Local Similarity 75.0%; Pred. No. 94;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LHDDLEA 9
 DB 202 VHDDLES 209

RESULT 6

C69226
 type I restriction modification enzyme, subunit M - Methanobacterium thermoautotrophicum

C:Species: Methanobacterium thermoautotrophicum
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C:Accession: C69226
 R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
 Qiu, D.; Spadafora, R.; Vicalte, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
 K.; S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 J. Bacteriol. 179, 7135-7155, 1997

A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
 A:Reference number: A69000; PMID:98037514; PMID:9371463

A:Accession: C69226
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-616 <MTH>
 A:Cross-references: UNIPROT:Q27025; UNIPARC:UPI000006673D; GB:AB000668; GB:AB000666; NID

A:Experimental source: strain Delta H

C:Genetics:
 A:Gene: MTH942

A:Start codon: GTG
 C:Superfamily: type I site-specific deoxyribonuclease chain hsdM

Query Match 77.8%; Score 35; DB 2; Length 616;
 Best Local Similarity 77.8%; Pred. No. 96;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHDDLEA 9
 DB 465 VLHDDLEA 473

RESULT 7

AB1316
 chemotaxis regulatory protein Cj1118c (imported) - Campylobacter jejuni (strain NCTC 111

C:Species: Campylobacter jejuni
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004

C:Accession: AB1316
 R:Parhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Baaham, D.; Chillin
 C.W.; Quail, M.; Randerdrem, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrel

Nature 403, 665-668, 2000
 A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp

A:Reference number: AB1250; PMID:20150912; PMID:10688204

A:Accession: AB1316
 A:Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-130 <PAR>

A:Cross-references: UNIPROT:P71129; UNIPARC:UPI00001277C0; GB:AL139077; GB:AL111166; NID
 A:Experimental source: serotype O2, strain NCTC 11168

C:Genetics:
 A:Gene: cheY, Cj1118c
 C:Superfamily: signal transduction receiver (phosphoacceptor) protein, CheY type; respon

Query Match 75.6%; Score 34; DB 2; Length 130;
 Best Local Similarity 85.7%; Pred. No. 26;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 2, 2006, 21:41:26 ; Search time 72 Seconds

(without alignments)
88.191 Million cell updates/sec

Title: US-10-623-176a-2

Perfect score: 45
Sequence: 1 VLHDDLRA 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	1136	2	06P189 HUMAN
2	40	88.9	571	2	06KZHS PICTO
3	39	86.7	668	2	06LZ81 METAP
4	38	84.4	1148	2	003897 YEAST
5	38	84.4	1176	2	05CSZ8 CRYEV
6	37	82.2	1131	2	08IYN3 HUMAN
7	37	82.2	1136	2	08HX84 HUMAN
8	37	82.2	1133	2	05RB40 PONFY
9	37	82.2	1165	2	092619 HUMAN
10	36	80.0	101	2	06AMV9 DESPS
11	36	80.0	231	2	06AUN7 ORYSA
12	36	80.0	253	2	04ZMT6 PSESY
13	36	80.0	585	2	08EJS9 SHRON
14	36	80.0	681	2	08P0R0 XANNC
15	36	80.0	694	2	05G0J3 XANOR
16	36	80.0	870	2	04PCT0 USTWA
17	36	80.0	1155	2	05QU07 IDILO
18	35	77.8	119	2	080057 9CAUD
19	35	77.8	120	2	08SCW6 9CAUD
20	35	77.8	148	2	06ZM54 HUMAN
21	35	77.8	268	2	04FVQ3 9GAMM
22	35	77.8	354	2	057F00 9TRYF
23	35	77.8	376	2	08MVB1 IXOSC
24	35	77.8	415	2	04QAS5 LBIWA
25	35	77.8	415	2	05GAD4 MAITZB
26	35	77.8	415	2	05GAD2 MAITZB
27	35	77.8	446	2	08SDK3 BPPND
28	35	77.8	496	2	09MBP0 9CAUD
29	35	77.8	549	2	05Y641 NOCPA
30	35	77.8	579	2	05NDE3 TETNG
31	35	77.8	590	2	05NDE4 FUGRU

32	35	77.8	603	1	VE1 HPV21	P50759 human papil
33	35	77.8	604	1	VE1 HPV19	Q02048 human papil
34	35	77.8	605	1	VE1 HPV14	P36721 human papil
35	35	77.8	616	2	O27025 MERTH	O27025 methanobact
36	35	77.8	843	2	O5ZKE4 CHICK	O5ZKE4 gallus gall
37	35	77.8	872	2	O8UHZ8 XENTR	O6JH28 gallus gall
38	35	77.8	952	2	O6D1R8 XENTR	O6D1R8 xenopus tro
39	35	77.8	952	2	O5KOU2 CRYNE	O5KOU2 cryptococcu
40	35	77.8	952	2	O5SP14 CRYNE	O5SP14 cryptococcu
41	35	77.8	1246	2	O4QHU5 LBIWA	O4QHU5 leishmania
42	34	75.6	68	2	O8EYR5 LEPIN	O8EYR5 leprospira
43	34	75.6	113	1	O5JNG1 ORYSA	O5JNG1 oryza sativ
44	34	75.6	130	1	CHRY CAMJ	P71129 campylobact
45	34	75.6	130	2	Q5HTY6 CAMJR	Q5HTY6 campylobact

ALIGNMENTS

RESULT 1
06P189 HUMAN
ID 06P189 HUMAN PRELIMINARY; PRT; 1136 AA.
AC 06P189;
DT 05-JUL-2004 (TRMBLrel. 27, Created)
DT 05-JUL-2004 (TRMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRMBLrel. 27, Last annotation update)
DE Minor histocompatibility antigen HA-1.
GN Name=HA-1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold R.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Scheiner C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusik A., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.U., Ustin T.B., Toshlyuk S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullishy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Fahy J., Heiton B., Kettelman M., Madan A., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywicki M.I., Skalska U., Smalls D.B.,
RA Scherch A., Schein J.B., Jones S.J.M., Maza M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Strausberg R.,
RA Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC065223; AAH65223.1; -; mRNA.
DR HSSP; C07960; IMA4.
DR GO; GO:0007242; P:intracellular signaling cascade; IRA.
DR InterPro; IPR001060; Cdc15_Pes_Cip4.
DR InterPro; IPR002219; DAG_P8-bind.
DR InterPro; IPR000198; RhoGAP.
DR Pfam; PF00130; C1_1; 1.
DR Pfam; PF00620; RhoGAP; 1.
DR PRINTS; PRO0008; DAGDEDMAIN.
DR SMART; SM00109; C1; 1.
DR SMART; SM0055; RCH; 1.


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DR SMART: SM00324; RhogAP; 1.
DR PROSITE; PS00479; DAG_BR_BIND_DOM_1; UNKNOWN_1.
DR PROSITE; PS50081; DAG_BR_BIND_DOM_2; 1.
DR PROSITE; PS50238; RHOGAP; 1.
SQ SEQUENCE 1136 AA; 124550 MW; 1487073296102DD5 CRC64;

Query Match 100.0%; Score 45; DB 2; Length 1136;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHDDLLEA 9
Db 137 VLHDDLLEA 145

RESULT 2
06KZHS PICTO PRELIMINARY; PRT; 571 AA.
ID 06KZHS PICTO PRELIMINARY; PRT; 571 AA.
AC 06KZHS_
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE Molybdopterin biosynthesis MoaA protein.
GN OrderedLocustNames=PT01292;
OS Picrophilus torridus;
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Picrophilaceae; Picrophilus.
OX NCBI_TaxID=82076;
RN [1]
NP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 9780 / ATCC 700027;
RX PubMed:15184674; DOI=10.1073/pnas.0401356101;
FA Fuetterer O., Angelov A., Liesegang H., Gottschalk G., Schleger C.,
FA Schepers B., Dock C., Antimikhan G., Liebl W.;
RT "Genome sequence of Picrophilus torridus and its implications for life
RT around pH 0.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9091-9096(2004).
DR EMBL; AB017261; AAT3877.1; -; Genomic_DNA.
DR GO; GO:0006777; P:Mo-molybdopterin cofactor biosynthesis; IEA.
DR InterPro; IPR001453; MoCF_bios.
DR InterPro; IPR005111; MoaA_C.
DR InterPro; IPR005110; MoaA_N.
DR Pfam; PF00994; MoCF_biosynth; 1.
DR Pfam; PF03454; MoaA_C; 1.
DR Pfam; PF03453; MoaA_N; 1.
DR ProDom; PD002460; MoCF_biosynth; 1.
DR TRFPAme; TIGR00177; molyb_syn; 1.
KV Complete proteome.
SQ SEQUENCE 571 AA; 64707 MW; D2E18BF6C15FA1 CRC64;

Query Match 88.9%; Score 40; DB 2; Length 571;
Best Local Similarity 88.9%; Pred. No. 69;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHDDLLEA 9
Db 63 VLHDDLLEA 71

RESULT 3
06L281 METMP PRELIMINARY; PRT; 668 AA.
ID 06L281 METMP PRELIMINARY; PRT; 668 AA.
AC 06L281;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE MCM family related protein.
GN OrderedLocustNames=MMP0748;
OS Methanococcus maripaludis.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanococcaceae; Methanococcus.
OX NCBI_TaxID=39152;
RN [1]

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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=S2 / IL;
RX PubMed:15466049; DOI=10.1128/JB.186.20.6956-6969.2004;
FA Hendrickson B.L., Kaul R., Zhou Y., Boyee D., Chapman P., Chung J.,
FA Conway de Macario E., Dodsworth J.A., Gillett W., Graham D.B.,
FA Hackett M., Haydock A.K., Kang A., Land M.L., Levy R., Lie T.J.,
FA Major T.A., Moore B.C., Porat I., Palmeliri A., Rouse G.,
FA Saenphimachak C., Seoll D., Van Dien S., Wang T., Whitman W.B.,
FA Xia Q., Zhang Y., Larimer F.W., Olson M.V., Leigh J.A.;
RT "Complete genome sequence of the genetically tractable
RT hydrogeotrophic methanogen Methanococcus maripaludis.";
RL J. Bacteriol. 186:6956-6969(2004).
DR EMBL; BX957221; CAZ30304.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0008094; F:DNA-dependent ATPase activity; IEA.
DR GO; GO:0006270; P:DNA replication initiation; IEA.
DR InterPro; IPR002048; EF_hand_Ca_bd.
DR Pfam; PF00493; MCM; 1.
DR Pfam; PF00493; MCM; 1.
DR PRINTS; PR01557; MCMFAMILY.
DR ProDom; PD001041; MCM; 1.
DR SMART; SM00350; MCM; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS50051; MCM_2; 1.
KV Complete proteome.
SQ SEQUENCE 668 AA; 75660 MW; 2ADAF3800B1049F4 CRC64;

Query Match 86.7%; Score 39; DB 2; Length 668;
Best Local Similarity 86.7%; Pred. No. 136+02;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHDDLLEA 9
Db 628 VLHDDLLEA 636

RESULT 4
003897 YEAST PRELIMINARY; PRT; 1148 AA.
ID 003897 YEAST PRELIMINARY; PRT; 1148 AA.
AC 003897;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN ORFNames=YDR128W;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Saccharomycetes; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
NP NUCLEOTIDE SEQUENCE.
RC STRAIN=AB972;
RA Oliver K., Harris D.;
RT Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AB972;
RA Barrall B., Rajandream M.A.;
RT Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
CC -1 INTERACTION:
CC P39079; CTF6; NbrExp-1; Intact=EBI-32422, EBI-19077;
DR EMBL; Z48179; CA888209.1; -; Genomic_DNA.
DR PIR; S51855; S51855.
DR Intact; Q03897; -.
DR Ensembl; YDR128W; Saccharomyces cerevisiae.
DR SGD; S000002535; YDR128W.
DR GO; GO:0003229; Cytoplasmic membrane (sensu Fungi); IDA.
DR InterPro; IPR006575; RMD.
DR Pfam; PF00400; WD40; 4.
DR PRINTS; PR00320; GPROTEINBRPT.
DR SMART; SM00591; RMD; 1.

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Title: US-10-623-176a-2

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Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	45	100.0	9	US-09-269-250B-20	Sequence 20, Appl
2	45	100.0	9	US-09-489-760-2	Sequence 2, Appl
3	45	100.0	13	US-09-269-250B-28	Sequence 28, Appl
4	45	100.0	13	US-09-489-760-16	Sequence 16, Appl
5	45	100.0	26	US-09-269-250B-36	Sequence 36, Appl
6	38	84.4	199	US-09-543-681A-7115	Sequence 7115, Ap
7	38	84.4	1148	US-09-538-092-156	Sequence 156, App
8	37	82.2	9	US-09-269-250B-18	Sequence 18, Appl
9	37	82.2	9	US-09-489-760-5	Sequence 5, Appl
10	37	82.2	13	US-09-269-250B-26	Sequence 26, Appl
11	37	82.2	13	US-09-489-760-14	Sequence 14, Appl
12	36	80.0	9	US-09-269-250B-29	Sequence 29, Appl
13	36	80.0	9	US-09-489-760-1	Sequence 1, Appl
14	35	77.8	608	US-09-252-991A-26210	Sequence 26210, A
15	35	77.8	789	US-09-107-532A-6734	Sequence 6734, Ap
16	34	75.6	435	US-09-270-767-33480	Sequence 33480, A
17	34	75.6	435	US-09-270-767-33480	Sequence 33480, A
18	34	75.6	446	US-09-270-767-48697	Sequence 48697, A
19	33	73.3	70	US-09-134-000C-3701	Sequence 3701, Ap
20	33	73.3	256	US-09-134-000C-4544	Sequence 4544, Ap
21	33	73.3	295	US-09-252-991A-24727	Sequence 24727, A
22	33	73.3	332	US-09-902-540-12129	Sequence 12129, A
23	33	73.3	341	US-09-252-991A-21448	Sequence 21448, A
24	33	73.3	342	US-09-818-780-97	Sequence 97, Appl
25	33	73.3	343	US-08-279-058B-9	Sequence 9, Appl
26	33	73.3	343	US-08-828-323-9	Sequence 9, Appl
27	33	73.3	343	US-08-828-323A-9	Sequence 9, Appl

28	33	73.3	352	US-09-489-039A-12951	Sequence 12951, A
29	33	73.3	627	US-09-710-279-1068	Sequence 1068, Ap
30	33	73.3	683	US-09-489-039A-9868	Sequence 9868, Ap
31	33	73.3	851	US-09-071-035-326	Sequence 326, App
32	33	73.3	851	US-09-071-035-330	Sequence 330, App
33	33	73.3	851	US-09-071-035-334	Sequence 334, App
34	33	73.3	851	US-10-206-576-326	Sequence 326, App
35	33	73.3	851	US-10-206-576-330	Sequence 330, App
36	33	73.3	851	US-10-206-576-334	Sequence 334, App
37	33	73.3	1554	US-09-252-991A-26814	Sequence 26814, A
38	33	73.3	1770	US-09-487-558B-298	Sequence 298, App
39	33	73.3	4150	US-09-428-517-2	Sequence 2, Appl
40	32	71.1	35	US-09-082-279B-454	Sequence 454, App
41	32	71.1	35	US-09-082-279B-455	Sequence 455, App
42	32	71.1	35	US-09-082-279B-456	Sequence 456, App
43	32	71.1	35	US-08-474-349A-481	Sequence 481, App
44	32	71.1	35	US-08-474-349A-482	Sequence 482, App
45	32	71.1	35	US-08-474-349A-483	Sequence 483, App

ALIGNMENTS

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RESULT 1
US-09-269-250B-20
; Sequence 20, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elise
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 9
; TYPB: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-09-269-250B-20

Query Match      100.0%; Score 45; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 VLHDDLRA 9
Db      1 VLHDDLRA 9

RESULT 2
US-09-489-760-2
; Sequence 2, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
; APPLICANT: Rijksuniversiteit Te Leiden
; APPLICANT: Goulmy, Elise A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Hard, Victor H
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/09/489,760
; CURRENT FILING DATE: 2000-01-21
; EARLIER APPLICATION NUMBER: PCT/NL98/00424
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 9
; TYPB: PRT
; ORGANISM: Histocompatibility antigen

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US-09-489-760-2

Query Match 100.0%; Score 45; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 V|H|D|D|L|E|A 9
DB 1 V|H|D|D|L|E|A 9

RESULT 3

US-09-269-250E-28
Sequence 28, Application US/09269250E
Patent No. 6830883
GENERAL INFORMATION:
APPLICANT: Goulmy, Elsa
TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
FILE REFERENCE: 58994
CURRENT APPLICATION NUMBER: US/09/269,250E
CURRENT FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.1
SEQ ID NO 28
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: PCR Product
US-09-269-250E-28

Query Match 100.0%; Score 45; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 V|H|D|D|L|E|A 9
DB 3 V|H|D|D|L|E|A 11

RESULT 4

US-09-489-760-16
Sequence 16, Application US/09489760
Patent No. 6878375
GENERAL INFORMATION:
APPLICANT: Rijksuniversiteit Te Leiden
APPLICANT: Goulmy, Elsa A.J.M
APPLICANT: Hunt, Donald F
APPLICANT: Hard, Victor H
TITLE OF INVENTION: The HA-1 Antigen
FILE REFERENCE: 2183-42850S
CURRENT APPLICATION NUMBER: US/09/489,760
CURRENT FILING DATE: 2000-01-21
EARLIER APPLICATION NUMBER: PCT/NL98/00424
EARLIER FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
LENGTH: 13
TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: HA-1+/
US-09-489-760-16

Query Match 100.0%; Score 45; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 V|H|D|D|L|E|A 9
DB 3 V|H|D|D|L|E|A 11

RESULT 5
US-09-269-250E-36
Sequence 36, Application US/09269250E
Patent No. 6830883
GENERAL INFORMATION:
APPLICANT: Goulmy, Elsa
TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
FILE REFERENCE: 58994
CURRENT APPLICATION NUMBER: US/09/269,250E
CURRENT FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.1
SEQ ID NO 36
LENGTH: 26
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: PCR Product
US-09-269-250E-36

Query Match 100.0%; Score 45; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.072;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 V|H|D|D|L|E|A 9
DB 16 V|H|D|D|L|E|A 24

RESULT 6

US-09-543-681A-7115
Sequence 7115, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 7115
LENGTH: 199
TYPE: PRT
ORGANISM: Proteus mirabilis
US-09-543-681A-7115

Query Match 84.4%; Score 38; DB 2; Length 199;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 V|H|D|D|L|E|A 9
DB 178 V|H|D|D|L|E|A 186

RESULT 7

US-09-538-092-156
Sequence 156, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Glaxo, Inc
APPLICANT: Manefield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: March 2, 2006, 21:43:37 ; Search time 71 Seconds
(without alignments)
52.964 Million cell updates/sec

Title: US-10-623-176a-2

Perfect score: 45
Sequence: 1 VLHDDLRA 9

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications AA Main:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	45	100.0	9	5 US-10-861-335-1	Sequence 1, Appl1
4	45	100.0	9	6 US-11-007-740-20	Sequence 20, Appl1
5	45	100.0	10	4 US-10-623-176-43	Sequence 43, Appl1
6	45	100.0	13	4 US-10-623-176-76	Sequence 76, Appl1
7	45	100.0	13	4 US-10-791-217-16	Sequence 16, Appl1
8	45	100.0	13	6 US-11-007-740-28	Sequence 28, Appl1
9	45	100.0	17	4 US-10-623-176-57	Sequence 57, Appl1
10	45	100.0	22	4 US-10-623-176-53	Sequence 53, Appl1
11	45	100.0	25	4 US-10-623-176-55	Sequence 55, Appl1
12	45	100.0	26	6 US-11-007-740-36	Sequence 36, Appl1
13	45	100.0	27	4 US-10-623-176-51	Sequence 51, Appl1
14	45	100.0	29	4 US-10-623-176-49	Sequence 49, Appl1
15	41	91.1	9	4 US-10-623-176-41	Sequence 41, Appl1
16	41	91.1	9	4 US-10-623-176-45	Sequence 45, Appl1
17	39	86.7	65	4 US-10-424-599-242306	Sequence 242306, Appl1
18	37	82.2	9	4 US-10-623-176-10	Sequence 10, Appl1
19	37	82.2	9	4 US-10-623-176-47	Sequence 47, Appl1
20	37	82.2	9	4 US-10-791-217-5	Sequence 5, Appl1
21	37	82.2	9	6 US-11-007-740-18	Sequence 18, Appl1
22	37	82.2	10	4 US-10-623-176-44	Sequence 44, Appl1
23	37	82.2	12	4 US-10-623-176-65	Sequence 65, Appl1
24	37	82.2	13	4 US-10-623-176-74	Sequence 74, Appl1
25	37	82.2	13	4 US-10-791-217-14	Sequence 14, Appl1
26	37	82.2	13	6 US-11-007-740-26	Sequence 26, Appl1
27	37	82.2	17	4 US-10-623-176-69	Sequence 69, Appl1

ALIGNMENTS

28	37	82.2	19	4	US-10-623-176-52	Sequence 52, Appl1
29	37	82.2	19	4	US-10-623-176-70	Sequence 70, Appl1
30	37	82.2	21	4	US-10-623-176-71	Sequence 71, Appl1
31	37	82.2	22	4	US-10-623-176-63	Sequence 63, Appl1
32	37	82.2	23	4	US-10-623-176-72	Sequence 72, Appl1
33	37	82.2	25	4	US-10-623-176-67	Sequence 67, Appl1
34	37	82.2	26	4	US-10-623-176-66	Sequence 66, Appl1
35	37	82.2	27	4	US-10-623-176-60	Sequence 60, Appl1
36	37	82.2	28	4	US-10-623-176-61	Sequence 61, Appl1
37	37	82.2	29	4	US-10-623-176-59	Sequence 59, Appl1
38	37	82.2	1136	4	US-10-072-012-280	Sequence 280, Appl1
39	37	82.2	1136	4	US-10-072-012-729	Sequence 729, Appl1
40	37	82.2	1165	4	US-10-072-012-730	Sequence 730, Appl1
41	36	80.0	9	4	US-10-623-176-1	Sequence 1, Appl1
42	36	80.0	9	4	US-10-623-176-40	Sequence 40, Appl1
43	36	80.0	9	4	US-10-791-217-1	Sequence 1, Appl1
44	36	80.0	9	6	US-11-007-740-29	Sequence 29, Appl1
45	36	80.0	10	4	US-10-623-176-6	Sequence 6, Appl1

RESULT 1
US-10-623-176-2
Sequence 2, Application US/10623176
Publication No. US20040092446A1
GENERAL INFORMATION:
APPLICANT: Goulety, Elie A.J.M.
APPLICANT: Hunt, Donald F.
TITLE OF INVENTION: HA-1 epitopes and uses thereof
FILE REFERENCE: 2183-604705
CURRENT FILING DATE: 2003-07-18
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: 09/489,760
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: EP 97202303.0
PRIOR FILING DATE: 1997-07-23
PRIOR APPLICATION NUMBER: PCT/NL98/00424
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: JP 2000-504165
PRIOR FILING DATE: 2000-01-24
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
NAME/KEY: SITE
LOCATION: (1) .. (9)
US-10-623-176-2
Query Match 100.0%; Score 45; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLHDDLRA 9
DB 1 VLHDDLRA 9
RESULT 2
US-10-791-217-2
Sequence 2, Application US/10791217
Publication No. US20040191268A1
GENERAL INFORMATION:
APPLICANT: Goulety, Elie A.J.M.
APPLICANT: Hunt, Donald F.
APPLICANT: Engelhard, Victor H

TITLE OF INVENTION: The HA-1 Antigen
FILE REFERENCE: 2183-4285US
CURRENT APPLICATION NUMBER: US/10/791,217
CURRENT FILING DATE: 2004-03-02
PRIOR APPLICATION NUMBER: US/09/489,760
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: PCT/NL98/00424
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: obtained from histocompatibility antigen
US-10-791-217-2

Query Match 100.0%; Score 45; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHDDLLEA 9
Db 1 VLHDDLLEA 9

RESULT 3
US-10-861-335-1
Sequence 1, Application US/10861335
Publication No. US20050031612A1
GENERAL INFORMATION:
APPLICANT: Goulmy, Elise A.J.M.
TITLE OF INVENTION: Minor histocompatibility antigen HA-1: target antigen for immunot
FILE REFERENCE: 2183-6479US
CURRENT APPLICATION NUMBER: US/10/861,335
CURRENT FILING DATE: 2004-06-04
PRIOR APPLICATION NUMBER: PCT/NL02/00791
PRIOR FILING DATE: 2002-12-05
PRIOR APPLICATION NUMBER: EP 01204704.9
PRIOR FILING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HA-1 peptide
US-10-861-335-1

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Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHDDLLEA 9
Db 1 VLHDDLLEA 9

RESULT 4
US-11-007-740-20
Sequence 20, Application US/11007740
Publication No. US2005023350A1
GENERAL INFORMATION:
APPLICANT: Goulmy, Elise
TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
FILE REFERENCE: 2799/58994-A
CURRENT APPLICATION NUMBER: US/11/007,740
CURRENT FILING DATE: 2004-12-08
PRIOR APPLICATION NUMBER: 09/269,250
PRIOR FILING DATE: 1999-05-21

NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-11-007-740-20

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Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHDDLLEA 9
Db 1 VLHDDLLEA 9

RESULT 5
US-10-623-176-43
Sequence 43, Application US/10623176
Publication No. US20040092446A1
GENERAL INFORMATION:
APPLICANT: Goulmy, Elise A.J.M.
APPLICANT: Hunt, Donald F.
TITLE OF INVENTION: HA-1 epitopes and uses thereof
FILE REFERENCE: 2183-6047US
CURRENT APPLICATION NUMBER: US/10/623,176
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/489,760
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: EP 97202303.0
PRIOR FILING DATE: 1997-07-23
PRIOR APPLICATION NUMBER: PCT/NL98/00424
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: JP 2000-504165
PRIOR FILING DATE: 2000-01-24
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 43
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
NAME/KEY: SITE
LOCATION: (1)..(10)
US-10-623-176-43

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Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHDDLLEA 9
Db 1 VLHDDLLEA 9

RESULT 6
US-10-623-176-76
Sequence 76, Application US/10623176
Publication No. US20040092446A1
GENERAL INFORMATION:
APPLICANT: Goulmy, Elise A.J.M.
APPLICANT: Engelhard, Victor H.
TITLE OF INVENTION: HA-1 epitopes and uses thereof
FILE REFERENCE: 2183-6047US
CURRENT APPLICATION NUMBER: US/10/623,176
CURRENT FILING DATE: 2003-07-18

GenCore version 5.1.7
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Title: US-10-623-176A-2

Perfect score: 45

Sequence: 1 VLHDDLRA 9

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Total number of hits satisfying chosen parameters: 135339

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Published Applications AA New:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	45	100.0	9	US-11-010-748A-11	Sequence 11, Appl
2	37	82.2	9	US-11-010-748A-12	Sequence 12, Appl
3	33	73.3	519	US-11-087-099-5406	Sequence 5406, Ap
4	33	73.3	519	US-11-087-099-9352	Sequence 9352, Ap
5	33	73.3	623	US-10-793-626-1068	Sequence 1068, Ap
6	32	71.1	297	US-11-092-140-9	Sequence 9, Appl
7	32	71.1	321	US-11-092-140-12	Sequence 12, Appl
8	32	71.1	324	US-11-098-686-10760	Sequence 10760, A
9	32	71.1	422	US-10-524-647-112	Sequence 122, App
10	32	71.1	422	US-10-524-972-110	Sequence 110, App
11	32	71.1	580	US-10-485-788A-516	Sequence 516, App
12	32	71.1	580	US-11-072-512-2876	Sequence 2876, Ap
13	32	71.1	737	US-11-152-366-28	Sequence 28, Appl
14	31	68.9	226	US-10-510-941-20	Sequence 20, Appl
15	31	68.9	304	US-11-156-084-281	Sequence 291, App
16	31	68.9	310	US-11-156-084-301	Sequence 301, App
17	31	68.9	315	US-11-156-084-313	Sequence 313, App
18	31	68.9	315	US-11-156-084-353	Sequence 353, App
19	31	68.9	443	US-11-098-686-10861	Sequence 10861, A
20	31	68.9	469	US-11-124-368A-336	Sequence 336, App
21	31	68.9	469	US-11-124-368A-337	Sequence 337, App
22	31	68.9	1254	US-10-528-031-47	Sequence 47, Appl
23	31	68.9	1445	US-11-169-041-181	Sequence 181, App
24	31	68.9	4128	US-10-770-726-77	Sequence 77, Appl
25	31	68.9	4868	US-11-044-111-24	Sequence 24, Appl

26	30	66.7	139	7	US-11-087-099-7123	Sequence 7123, Ap
27	30	66.7	161	7	US-11-200-394-17	Sequence 17, Appl
28	30	66.7	345	7	US-11-087-099-3274	Sequence 3274, Ap
29	30	66.7	365	7	US-11-087-099-4866	Sequence 4866, Ap
30	30	66.7	386	7	US-11-087-099-12026	Sequence 12026, A
31	30	66.7	439	7	US-11-087-099-739	Sequence 739, App
32	30	66.7	439	7	US-11-087-099-2428	Sequence 2428, Ap
33	30	66.7	468	6	US-10-957-566-28	Sequence 28, Appl
34	30	66.7	468	7	US-11-097-589-26	Sequence 26, Appl
35	30	66.7	696	7	US-11-018-868-51	Sequence 51, Appl
36	30	66.7	1210	6	US-10-624-932-26	Sequence 26, Appl
37	30	66.7	1213	7	US-11-039-398-14	Sequence 14, Appl
38	30	66.7	1216	7	US-11-039-398-12	Sequence 12, Appl
39	30	66.7	1219	7	US-11-039-398-10	Sequence 10, Appl
40	30	66.7	1222	7	US-11-039-398-8	Sequence 8, Appl
41	30	66.7	1232	7	US-11-039-398-18	Sequence 18, Appl
42	30	66.7	1235	7	US-11-039-398-16	Sequence 16, Appl
43	30	66.7	1249	7	US-11-039-398-22	Sequence 22, Appl
44	30	66.7	1252	7	US-11-039-398-20	Sequence 20, Appl
45	30	66.7	1552	6	US-10-330-773-941	Sequence 941, App

ALIGNMENTS

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RESULT 1
US-11-010-748A-11
; Sequence 11, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMATTER, Wolfgang
; APPLICANT: MOLL, Heidrun
; APPLICANT: SCHARM, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(9)
; OTHER INFORMATION: Human minor histocompatibility antigens HA-1 characterized by T c
; OTHER INFORMATION: ell epitopes
US-11-010-748A-11

Query Match          100.0%; Score 45; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHDDLRA 9
DB 1 VLHDDLRA 9

RESULT 2
US-11-010-748A-12
; Sequence 12, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMATTER, Wolfgang
; APPLICANT: MOLL, Heidrun
; APPLICANT: SCHARM, Burkhard

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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
 FILE REFERENCE: MER-136
 CURRENT APPLICATION NUMBER: US/11/010,748A
 PRIOR FILING DATE: 2004-12-13
 PRIOR APPLICATION NUMBER: PCT/EP03/06251
 PRIOR FILING DATE: 2003-06-13
 PRIOR APPLICATION NUMBER: EP02013423.5
 PRIOR FILING DATE: 2002-06-13
 NUMBER OF SEQ ID NOS: 926
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 12
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: MISC FEATURE
 LOCATION: (1)..(9)
 OTHER INFORMATION: Human minor histocompatibility antigens HA-1 characterized by T c
 OTHER INFORMATION: ell epitopes
 US-11-010-748A-12

Query Match 82.2%; Score 37; DB 7; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1e+05;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLHDDLEA 9
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 Db 1 VLHDDLEA 9

RESULT 3
 US-11-087-099-5406
 Sequence 5406, Application US/11087099
 Publication No. US20060041961A1
 GENERAL INFORMATION:
 APPLICANT: Abad, Mark S. et al.
 TITLE OF INVENTION: Genes and Uses for Plant Improvement
 FILE REFERENCE: 38-21(53450)B EP
 CURRENT APPLICATION NUMBER: US/11/087,099
 CURRENT FILING DATE: 2005-03-22
 NUMBER OF SEQ ID NOS: 12464
 SEQ ID NO 5406
 LENGTH: 519
 TYPE: PRT
 ORGANISM: Candida apicola
 US-11-087-099-5406

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 Best Local Similarity 75.0%; Pred. No. 69;
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Qy 1 VLHDDLE 8
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 Db 63 MLHDDVLE 70

RESULT 4
 US-11-087-099-9352
 Sequence 9352, Application US/11087099
 Publication No. US20060041961A1
 GENERAL INFORMATION:
 APPLICANT: Abad, Mark S. et al.
 TITLE OF INVENTION: Genes and Uses for Plant Improvement
 FILE REFERENCE: 38-21(53450)B EP
 CURRENT APPLICATION NUMBER: US/11/087,099
 CURRENT FILING DATE: 2005-03-22
 NUMBER OF SEQ ID NOS: 12464
 SEQ ID NO 9352
 LENGTH: 519
 TYPE: PRT
 ORGANISM: Candida apicola
 US-11-087-099-9352

Query Match 73.3%; Score 33; DB 7; Length 519;
 Best Local Similarity 100.0%; Pred. No. 69;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HDDLE 8
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 Db 65 HDDLE 70

RESULT 5
 US-10-793-626-1068
 Sequence 1068, Application US/10793626
 Publication No. US20050255478A1
 GENERAL INFORMATION:
 APPLICANT: KIMBERLY, WILLIAM JOHN
 TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 FILE REFERENCE: P03480US
 CURRENT APPLICATION NUMBER: US/10/793,626
 CURRENT FILING DATE: 2004-03-04
 PRIOR APPLICATION NUMBER: 60/164,258
 PRIOR FILING DATE: 1999-11-09
 NUMBER OF SEQ ID NOS: 4472
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 1068
 LENGTH: 623
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: synthetic
 OTHER INFORMATION: amino acid sequence
 US-10-793-626-1068

Query Match 73.3%; Score 33; DB 6; Length 623;
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Qy 1 VLHDDLEA 9
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 Db 606 VVHDKLEA 614

RESULT 6
 US-11-092-140-9
 Sequence 9, Application US/11092140
 Publication No. US20050262590A1
 GENERAL INFORMATION:
 APPLICANT: Subramaniam, S.; Slater, S.; Karberg, K.; Chen, R.; Valentin, H.; Wong, Y.
 TITLE OF INVENTION: Nucleic Acid Sequences to Proteins Involved in Tocopherol Synthes
 FILE REFERENCE: 16515.054
 CURRENT APPLICATION NUMBER: US/11/092,140
 CURRENT FILING DATE: 2005-03-29
 PRIOR APPLICATION NUMBER: US/09/688,069
 PRIOR FILING DATE: 2000-10-14
 NUMBER OF SEQ ID NOS: 114
 SEQ ID NO 9
 LENGTH: 297
 TYPE: PRT
 ORGANISM: Arabidopsis sp.
 US-11-092-140-9

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 Best Local Similarity 62.5%; Pred. No. 58;
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Qy 1 VLHDDLE 8
 :|||:
 Db 77 LHDDVD 84

RESULT 7
 US-11-092-140-12
 Sequence 12, Application US/11092140
 Publication No. US20050262590A1

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 2, 2006, 21:44:02 ; Search time 79 Seconds

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Title: US-10-623-176a-2

Sequence: 1 VLHDDLRA 9

Scoring table: BLOSUM62

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Total number of hits satisfying chosen parameters: 401289

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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9: geneseqp2005s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	37	82.2	9	2	AAW99197	Aaw99197 Minor his
5	37	82.2	9	2	AAW97374	Aaw97374 HA-1 R-al
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11	28	62.2	9	2	AAW10132	Aaw10132 T cell ep
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13	28	62.2	9	8	ADK68732	Adk68732 Epitope 1
14	28	62.2	9	8	ADK05291	Adk05291 Hepatitis
15	28	62.2	9	8	ADK05293	Adk05293 Hepatitis
16	28	62.2	9	8	ADQ10530	Adq10530 Cercopith
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34	25	55.6	9	4	AAW97144	Aaw97144 Amino ter
35	25	55.6	9	4	AAW84492	Aaw84492 Peptide f
36	25	55.6	9	5	AAE26631	Aae26631 Yeast GPA
37	25	55.6	9	7	ADC25889	Adc25889 Yeast GPA
38	24	53.3	6	2	AAW99196	Aaw99196 Endothel
39	24	53.3	7	2	AAW99140	Aaw99140 Endothel
40	24	53.3	7	2	AAW33386	Aaw33386 Altered I
41	24	53.3	7	4	AAW70589	Aaw70589 Human imm
42	24	53.3	7	5	AAO21066	Aao21066 Isomerise
43	24	53.3	7	5	AAE28095	Aae28095 Human imm
44	24	53.3	8	8	ADT39474	Adt39474 hSARS vitr
45	24	53.3	8	8	ADT39474	Adt39474 hSARS vitr

ALIGNMENTS

RESULT 1
ID AAW99196 standard; peptide; 9 AA.
XX
XX AAW99196;
AC
DT 20-MAY-1999 (first entry)
XX
DB Minor histocompatibility antigen HA-1 T-cell epitope #2.
DB
XX Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
KW graft versus host disease; bone marrow transplant; leukaemia; vaccine;
XX diagnosis; aplastic anaemia; immune deficiency disease.
XX
OS Homo sapiens.
XX
XX
PN WO9905174-A1.
XX
PD 04-FEB-1999.
XX
PF 23-JUL-1998; 98WO-NL000425.
XX
PR 23-JUL-1997; 97EP-0020303.
XX
XX (UYLE-) RIKSDNIV LEIDEN.
XX
PI Goulimy EAJM, Hunt DF, Engelhard VH;
XX WPI; 1999-153312/13.
XX
XX A new minor histocompatibility antigen, HA-1 - useful to treat immune
PT diseases and prevent rejection and host versus graft disease in bone
PT marrow and organ transplantation.
XX
XX Claim 3; Page 32; 47pp; English.
PS
XX The present sequence represents a new peptide (P1) constituting a T-cell
CC epitope obtainable from the minor histocompatibility antigen HA-1. The
CC peptide is immunogenic and can be used as part of a vaccine. P1 is used
CC as a medicine, to induce tolerance for transplants, prevent rejection
CC and/or graft versus host disease, or to treat (auto) immune diseases. In
CC particular it can be used with bone marrow transplantation, in the
CC treatment of severe aplastic anaemia, leukaemia, and immune deficiency
XX diseases
XX
XX Sequence 9 AA;
SQ

Query Match 100.0%; Score 45; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHDDLLEA 9
 |||||
 Db 1 VLHDDLLEA 9

RESULT 2

AAW97375
 ID AAW97375 standard; protein; 9 AA.

AC AAW97375;

DT 13-MAY-1999 (first entry)

DE HA-1 H-allele sequence.

KM Intron; minor histocompatibility antigen HA-1; typing allele; H allele;

KW R allele; polymorphic nucleotide; HA-1 typing; bone marrow transplant;

XX severe aplastic anaemia; leukaemia; immune deficiency disease; ss.

OS Homo sapiens.

PN WO9905313-A2.

PD 04-FEB-1999.

PF 23-JUL-1998; 98WO-EP004928.

PR 23-JUL-1997; 97EP-00202303.

PR 02-JUN-1998; 98EP-00870125.

XX (UYLE-) RIJXSUNIV LEIDEN.

PI Goujmy B;

DR WPI; 1999-142960/12.

XX Typing minor histocompatibility antigen HA-1 - by amplifying and

PT identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection

PT of genetic aberrances.

PS Claim 18; Fig 5; 59pp; English.

XX The present sequence represents part of the minor histocompatibility

CC antigen HA-1 H-allele. The specification describes methods for typing

CC alleles (preferably the H and R alleles) of the minor histocompatibility

CC antigen HA-1 in a sample, which comprise detecting polymorphic

CC nucleotides in the cDNA or genomic nucleic acids of the alleles. The

CC methods can be used for HA-1 typing for bone marrow transplants, severe

CC aplastic anaemia, leukaemia and immune deficiency diseases, as well as

CC detection of genetic aberrances. The probes and primers of the invention

CC can be used to screen for the HA-1 alleles. The HA-1 peptides can be used

CC anti-idiotypic B cells and/or T cells and antibodies

XX SQ Sequence 9 AA;

Qy Query Match 100.0%; Score 45; DB 2; Length 9;

Db Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 11-MAR-2004 (first entry)

DT Human minor histocompatibility antigen HA-1 T cell epitope.

DE human; cytostatic; vaccine; SNP profile; cancer; leukaemia;

KW minor histocompatibility antigen; mRNA; T cell epitope.

XX minor histocompatibility antigen; mRNA; T cell epitope.

XX Homo sapiens.

PN WO2003106692-A2.

PD 24-DEC-2003.

PF 13-JUN-2003; 2003WO-EP006251.

PR 13-JUN-2002; 2002EP-00013423.

XX (MERK) MERCK PATENT GMBH.

PI Strickmatter W, Moll H;

DR WPI; 2004-082200/08.

XX Providing allelic variant epitope of protein based on single nucleotide

PT polymorphism by defining target protein, screening database of protein,

PT identifying, selecting allelic variant protein, creating variant

PT epitopes.

PS Disclosure; Page 82; 119pp; English.

XX The invention relates to a novel method for providing epitopes of allelic

CC variants of antigenic proteins from specific species based on single

CC nucleotide polymorphism (SNP), by defining target protein/peptide or its

CC subset, screening database of DNA encoding target protein, identifying,

CC selecting allelic peptide/protein variants, expression product or its

CC fragment encoded by DNA sequence having SNP, creating variant epitopes,

CC selecting epitopes binding to MHC protein. A protein of the invention has

CC cytostatic activity, and may have a use in a vaccine. The method is

CC useful for generating a SNP profile of one or more individuals from a

CC given species by applying the method for several protein from the

CC individuals, where the SNP profile was related to disease, preferably

CC cancer. This is useful for diagnosing a disease in an individual by

CC generating the SNP-related polymorphic profile. A method of the invention

CC is useful for transplanting hematopoietic stem cells from a donor to a

CC recipient and treating cancer, preferably leukaemia, and for determining

CC the progression, regression or onset of a treated disease. The present

CC sequence is used in the exemplification of the invention.

XX SQ Sequence 9 AA;

Qy Query Match 100.0%; Score 45; DB 8; Length 9;

Db Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHDDLLEA 9
 |||||
 Db 1 VLHDDLLEA 9

RESULT 4

AAW9197

ID AAW9197 standard; peptide; 9 AA.

AC AAW9197;

DT 20-MAY-1999 (first entry)

DE Minor histocompatibility antigen HA-1 T-cell epitope #3.

KW Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;

XX graft versus host disease; bone marrow transplant; leukaemia; vaccine;

XX diagnosis; aplastic anaemia; immune deficiency disease.

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 2, 2006, 21:44:37 ; Search time 20 Seconds
(without alignments)
43.298 Million cell updates/sec

Title: US-10-623-176a-2

Perfect score: 45

Sequence: 1 VLHDDLRA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 791

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	40.0	7	2	146868
2	17	37.8	9	2	S55696
3	16	35.6	7	2	P00663
4	16	35.6	7	2	S68004
5	16	35.6	8	2	PC4131
6	15	33.3	6	2	S78764
7	15	33.3	7	2	A59489
8	14	31.1	7	2	S20446
9	14	31.1	8	2	XGHU8U
10	14	31.1	9	2	AI2872
11	14	31.1	9	2	SI0920
12	14	31.1	9	2	A60427
13	13	28.9	8	2	A61328
14	13	28.9	9	2	PH0942
15	13	26.7	4	2	I40697
16	12	26.7	5	2	PT0679
17	12	26.7	5	2	PT0601
18	12	26.7	6	2	B35640
19	12	26.7	6	2	PT0533
20	12	26.7	7	2	A34026
21	12	26.7	7	2	B39040
22	12	26.7	7	2	PT0628
23	12	26.7	7	2	PT0722
24	12	26.7	7	2	PT0576
25	12	26.7	8	2	PT0368
26	12	26.7	8	2	PN0043
27	12	26.7	8	2	PT0557
28	12	26.7	9	2	A60108
29	12	26.7	9	2	PM0002

ALIGNMENTS

30	12	26.7	9	2	S65913	pyrimidine syntheses
31	12	26.7	9	2	PH0108	late G1-69 protein
32	12	26.7	9	2	PT0562	T-cell receptor be
33	12	26.7	9	2	B30572	T-cell receptor be
34	11	24.4	5	2	C41225	copper resistance
35	11	24.4	5	2	T10954	hypothetical prote
36	11	24.4	6	2	T11779	phosphoglycerate t
37	11	24.4	7	2	S25266	p1le protein - Esc
38	11	24.4	7	2	PT0246	Ig heavy chain CRD
39	11	24.4	8	2	S22428	chitin-binding pro
40	11	24.4	8	2	B33099	158k exoantigen -
41	11	24.4	8	2	S69165	ferredoxin a2 - Ja
42	11	24.4	9	2	S66419	tetrameric protein
43	11	24.4	9	2	PT0272	Ig heavy chain CRD
44	11	24.4	9	2	AI1497	transaldolase (EC
45	11	24.4	9	2	B39504	octamer-binding pr

RESULT 1

146868
alpha-myosin heavy chain - rabbit (fragment)
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
C/Accession: I46868
R/Friedman, D.J.; Umeda, P.K.; Sinha, A.M.; Hsu, H.
Proc. Natl. Acad. Sci. U.S.A. 81, 3044-3048, 1984
A/Title: Characterization of genomic clones specifying rabbit alpha- and beta-ventricul.
A/Reference number: I46868; MUID:84221501; PMID:6328491
A/Accession: I46868
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-7 <FRI>
A/Cross-references: UNIPROT:Q28742; UNIPARC:UPI0000087938; GB:K01698; NID:g165538; PIDN

Query Match
Best Local Similarity 40.0%; Score 18; DB 2; Length 7;

Matches 2; Conservativity 50.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;

QY 2 LHDD 5
:|:|:
DB 3 MHDD 6

RESULT 2

S55696
phosphoenolpyruvate carboxylase - Trypanosoma brucei

C/Species: Trypanosoma brucei
C/Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004

C/Accession: S55696
R/Hunt, M.; Koehler, P.

Biochim. Biophys. Acta 1249, 15-22, 1995
A/Title: Purification and characterization of phosphoenolpyruvate carboxylase from Try

A/Reference number: S55696; MUID:95284106; PMID:7766679

A/Status: preliminary
A/Molecule type: protein

A/Residues: 1-9 <HUN>
A/Cross-references: UNIPROT:Q7M355; UNIPARC:UPI000017B599

Query Match
Best Local Similarity 37.8%; Score 17; DB 2; Length 9;

Matches 2; Conservativity 33.3%; Pred. No. 2.8e+05; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHDDL 6
:|:|:
DB 3 ITHKXL 8

RESULT 3
P00663

membrane protein - porcine epidemic diarrhea virus (isolate Belgian CV777) (fragment)
 C:Species: porcine epidemic diarrhea virus
 C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 08-Oct-1999
 C:Accession: PQ0663
 R:Bridgen, A.; Duarte, M.; Tobler, K.; Laude, H.; Ackermann, M.
 J. Gen. Virol. 74, 1795-1804, 1993
 A:Title: Sequence determination of the nucleocapsid protein gene of the porcine epidemic
 A:Reference number: J02191; MUID:93389433; PMID:8397280
 A:Accession: PQ0663
 A:Molecule type: mRNA
 A:Residues: 1-7 <BRI>
 A:Cross-references: UNIPARC:UPI0000170PAC; GB:Z14976; NID:G311650; PIDN:CAA78699.1; PID:
 C:Comment: This virus is coronavirus related to human coronavirus 229E.
 C:Keywords: membrane protein

Query Match 35.6%; Score 16; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLH 3
 |||
 Db 3 VLH 5

RESULT 4
 S68004
 huco1in, 75K chain - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
 C:Accession: S68004
 R:Bggar, P.P.
 FEBS Lett. 375, 159-161, 1995
 A:Title: Huco1in, a new corticosteroid-binding protein from human plasma with structural
 A:Reference number: S68004; MUID:96087107; PMID:7498469
 C:Accession: S68004
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-7 <BDG>
 A:Cross-references: UNIPARC:UPI000017C164

Query Match 35.6%; Score 16; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDL 6
 |||
 Db 4 DDL 6

RESULT 5
 PC4131
 hypothetical protein 8 [imported] - Pseudomonas aeruginosa (fragment)
 C:Species: Pseudomonas aeruginosa
 C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 31-Dec-2004
 C:Accession: PC4131
 R:Kawasaki, S.; Arai, H.; Igarashi, Y.; Kodama, T.
 Gene 167, 87-91, 1995
 A:Title: Sequencing and characterization of the downstream region of the genes encoding
 A:Reference number: J04552; MUID:96144254; PMID:8566017
 A:Accession: PC4131
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-8 <KAW>
 A:Cross-references: UNIPROT:P95412; UNIPARC:UPI000017A96A; DDBJ:DS0473; NID:G1217594
 A:Note: This ORF is not annotated in GenBank entry P8BNRC, release 113.0
 C:Superfamily: Pseudomonas stutzeri nrd protein

Query Match 35.6%; Score 16; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDL 6
 |||
 Db 2 DDL 4

RESULT 6
 S78764
 ribosomal protein MRP-S23, mitochondrial - bovine (fragment)
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C:Accession: S78764
 R:Grack, H.R.
 submitted to the Protein Sequence Database, July 1999
 A:Reference number: S78760
 A:Accession: S78764
 A:Molecule type: protein
 A:Residues: 1-6 <GRA>
 A:Cross-references: UNIPARC:UPI000017C570
 C:Keywords: mitochondrial
 P:1-6/Product: ribosomal protein MRP-S23 (fragment) #status experimental <MAT>

Query Match 33.3%; Score 15; DB 2; Length 6;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LHDD 5
 |||
 Db 1 LHVD 4

RESULT 7
 A59489
 protein kinase C inhibitor - rat (fragment)
 C:Species: Rattus norvegicus
 C:Date: 25-Aug-2003 #sequence_revision 25-Aug-2003 #text_change 25-Aug-2003
 C:Accession: A59489
 R:Negoro, M.
 submitted to the Protein Sequence Database, June 2003
 A:Description: Purification of PKC from rat liver.
 A:Reference number: A59489
 A:Accession: A59489
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-7 <NEG>
 A:Experimental source: strain Wistar, liver
 A:Note: p-Hydroxyacetophenone-Sepharose binding protein

Query Match 33.3%; Score 15; DB 2; Length 7;
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VLHDD 5
 : |||
 Db 2 IFDD 6

RESULT 8
 S20446
 elastase - Pseudomonas aeruginosa
 C:Species: Pseudomonas aeruginosa
 C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 24-Jul-1997
 C:Accession: S20446
 R:Kessler, B.; Saffin, M.; Peretz, M.; Burshtein, Y.
 FEBS Lett. 299, 291-293, 1992
 A:Title: Identification of cleavage sites involved in proteolytic processing of Pseudomo
 A:Reference number: S20446; MUID:92183956; PMID:1544509
 A:Accession: S20446
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-7 <KES>
 A:Cross-references: UNIPARC:UPI000017A95F

Query Match 31.1%; Score 14; DB 2; Length 7;

OS Escherichia coli K12.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OC NCBI_TaxID=83333;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=82275057; PubMed=7051000;
 RA Parza C.D., Karels M.J., Navre M., Schachman H.K.;
 RT "Genes encoding Escherichia coli aspartate transcarbamoylase: the
 RT pyB-pyT operon."
 RL Proc. Natl. Acad. Sci. U.S.A. 79:4020-4024(1982).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=83195078; PubMed=6302686;
 RA Hoover T.A., Roof W.D., Foltermann K.F., O'Donovan G.A., Bencini D.A.,
 RA Wild J.R.;
 RT "Nucleotide sequence of the structural gene (pyrB) that encodes the
 RT catalytic polypeptide of aspartate transcarbamoylase of Escherichia
 RL coli."
 RL Proc. Natl. Acad. Sci. U.S.A. 80:2462-2466(1983).
 DR EMBL; J01670; AAA24475.1; -; Genomic_DNA.
 FT NON_TER
 SQ SEQUENCE 9 AA; 1085 MW; 99EFD723344AA1F1 CRC64;

Query Match 42.2%; Score 19; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 2.2e+06;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HDDDL 8
 :|:|:
 DB 3 HDNKLQ 8

RESULT 3
 ID 028742 RABIT PRELIMINARY; PRT; 7 AA.
 AC 028742
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Alpha-myosin heavy chain (Fragment).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
 OC Oryctolagus.
 OC NCBI_TaxID=9986;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=84221901; PubMed=6328491;
 RA Friedman P.J., Umeda P.K., Sima A.M., Hsu H.J., Jokovic S.,
 RA Rabinowitz M.;
 RT "Characterization of genomic clones specifying rabbit alpha- and beta-
 RT ventricular myosin heavy chains."
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).
 DR EMBL; K01698; AAA31415.1; -; Genomic_DNA.
 DR PIR; I46868; I46868.1
 FT NON_TER
 SQ SEQUENCE 7 AA; 916 MW; 6B1B1AA1B9326B0 CRC64;

Query Match 40.0%; Score 18; DB 2; Length 7;
 Best Local Similarity 50.0%; Pred. No. 2.2e+06;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LHDD 5
 :|:|:
 DB 3 WHDE 6

RESULT 4
 ID 07M355 9TRYP PRELIMINARY; PRT; 9 AA.
 AC 07M355
 DT 01-MAR-2004 (TREMBLrel. 26, Created)

DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Phosphoenolpyruvate carboxykinase.
 OS Trypanosoma brucei.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 OC NCBI_TaxID=56591;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=95284106; PubMed=7766679; DOI=10.1016/0167-4838(95)00061-X;
 RA Hunt W., Koehler P.;
 RT "Purification and characterization of phosphoenolpyruvate
 RT carboxykinase from Trypanosoma brucei."
 RL Biochim. Biophys. Acta 1249:15-22(1995).
 DR PIR; S55696; S55696.
 SQ SEQUENCE 9 AA; 1063 MW; 35F2244331B05047 CRC64;

Query Match 37.8%; Score 17; DB 2; Length 9;
 Best Local Similarity 33.3%; Pred. No. 2.2e+06;
 Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHDDL 6
 :|:|:
 DB 3 IIRKML 8

RESULT 5
 ID 099182 9SMEG PRELIMINARY; PRT; 7 AA.
 AC 099182
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Cytochrome oxidase I (Fragment).
 GN Name=COI;
 OS Gnathoclebias zonatus.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neocleosteii;
 OC Acanthomorphi; Acanthopterygii; Percomorphi; Atherinomorpha;
 OC Cyprinodontiformes; Aplocheilidae; Rivulinae; Gnathoclebias.
 OC NCBI_TaxID=135316;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20072828; PubMed=10603257; DOI=10.1006/mpcv.1999.0656;
 RA Murphy W.T., Thomsen J.E., Collier G.E.;
 RT "Phylogeny of the Neotropical Killifish Family Rivuliidae
 RT (Cyprinodontiformes, Aplocheilidae) inferred from mitochondrial DNA
 RT sequences."
 RL Mol. Phylogenet. Evol. 13:289-301(1999).
 DR EMBL; AF002591; AAD01074.1; -; Genomic_DNA.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER
 SQ SEQUENCE 7 AA; 899 MW; 672721F6CB572030 CRC64;

Query Match 35.6%; Score 16; DB 2; Length 7;
 Best Local Similarity 42.9%; Pred. No. 2.2e+06;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VLHDDL 7
 :|:|:
 DB 1 ILYQHL 7

RESULT 6
 ID 07Z6G0 HUMAN PRELIMINARY; PRT; 8 AA.
 AC 07Z6G0
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Fumarate hydratase (Fragment).
 OS Homo sapiens (Human).

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 2, 2006, 21:45:17 ; Search time 25 Seconds
(without alignments)
29.763 Million cell updates/sec

Title: US-10-623-176A-2

Perfect score: 45

Sequence: 1 VHDDLLEA 9

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 111694

Minimum DB seq length: 0
Maximum DB seq length: 99

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents AA:*

1: /cgn2_6/prodata/1/1aa/5 COMB.pep:.*
2: /cgn2_6/prodata/1/1aa/6 COMB.pep:.*
3: /cgn2_6/prodata/1/1aa/H COMB.pep:.*
4: /cgn2_6/prodata/1/1aa/PCUTUS COMB.pep:.*
5: /cgn2_6/prodata/1/1aa/RR COMB.pep:.*
6: /cgn2_6/prodata/1/1aa/Backfillseq.pep:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	9	2	US-09-269-2508-20
2	45	100.0	9	2	US-09-489-760-2
3	37	82.2	9	2	US-09-269-2508-18
4	37	82.2	9	2	US-09-489-760-5
5	36	80.0	9	2	US-09-269-2508-29
6	36	80.0	9	2	US-09-489-760-1
7	30	66.7	9	2	US-09-489-760-4
8	28.5	63.3	9	2	US-09-269-2508-38
9	25	55.6	7	2	US-09-025-819-5
10	25	55.6	7	2	US-09-808-126-5
11	25	55.6	7	2	US-09-803-951-5
12	25	55.6	9	2	US-08-582-333A-3
13	25	55.6	9	2	US-09-305-923A-7
14	25	55.6	9	2	US-08-946-298-4
15	23	51.1	6	2	US-09-217-609A-8
16	23	51.1	6	2	US-08-873-235B-8
17	23	51.1	5	2	US-08-159-339A-370
18	22	48.9	5	2	US-08-811-463-30
19	22	48.9	5	2	US-09-933-497B-30
20	22	48.9	7	1	US-08-208-036-7
21	22	48.9	7	1	US-08-208-036-9
22	22	48.9	7	1	US-08-428-823-7
23	22	48.9	7	1	US-08-428-823-9
24	22	48.9	7	2	US-08-556-419-14
25	22	48.9	7	2	US-09-173-941-82
26	22	48.9	7	2	US-09-494-190-82
27	22	48.9	8	1	US-08-403-378B-13

28	22	48.9	9	2	US-09-217-609A-11	Sequence 11, Appl
29	22	48.9	9	2	US-08-873-235B-11	Sequence 11, Appl
30	21	46.7	6	1	US-08-459-568-20	Sequence 20, Appl
31	21	46.7	6	1	US-08-399-411-20	Sequence 20, Appl
32	21	46.7	6	2	US-08-516-859A-20	Sequence 20, Appl
33	21	46.7	6	2	US-09-586-472-20	Sequence 20, Appl
34	21	46.7	6	2	US-09-528-706-20	Sequence 20, Appl
35	21	46.7	8	1	US-08-459-568-75	Sequence 20, Appl
36	21	46.7	8	1	US-08-399-411-75	Sequence 20, Appl
37	21	46.7	8	2	US-08-516-859A-75	Sequence 20, Appl
38	21	46.7	8	2	US-09-419-826-1	Sequence 20, Appl
39	21	46.7	8	2	US-09-419-826-37	Sequence 20, Appl
40	21	46.7	8	2	US-09-586-472-75	Sequence 20, Appl
41	21	46.7	9	1	US-09-528-706-75	Sequence 20, Appl
42	21	46.7	9	1	US-07-671-757-30	Sequence 20, Appl
43	21	46.7	9	1	US-08-343-602-2	Sequence 20, Appl
44	21	46.7	9	1	US-08-459-568-72	Sequence 20, Appl
45	21	46.7	9	1	US-08-459-568-78	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-09-269-2508-20
Sequence 20, Application US/092692508
Patent No. 6830883
GENERAL INFORMATION:
APPLICANT: Goulmy, Elia
TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
FILE REFERENCE: 58994
CURRENT APPLICATION NUMBER: US/09/269,2508
CURRENT FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patent in version 3.1
SEQ ID NO 20
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-09-269-2508-20

Query Match
Best Local Similarity 100.0%; Score 45; DB 2; Length 9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHDDLLEA 9
Db 1 VHDDLLEA 9

RESULT 2
US-09-489-760-2
Sequence 2, Application US/09489760
Patent No. 6878375
GENERAL INFORMATION:
APPLICANT: Rijksuniversiteit Te Leiden
APPLICANT: Goulmy, Elia A.J.M
APPLICANT: Hunt, Donald F
APPLICANT: Hard, Victor H
TITLE OF INVENTION: The HA-1 Antigen
FILE REFERENCE: 2183-428508
CURRENT APPLICATION NUMBER: US/09/489,760
CURRENT FILING DATE: 2000-01-21
EARLIER APPLICATION NUMBER: PCT/NL98/00424
EARLIER FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 2
LENGTH: 9
TYPE: PRT
ORGANISM: Histocompatibility antigen

US-09-489-760-2

Query Match 100.0%; Score 45; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 4.6e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLAHDDLLEA 9
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 DB 1 VLAHDDLLEA 9

RESULT 3
 US-09-269-250E-18
 ; Sequence 18, Application US/09269250E
 ; Patent No. 6830883
 ; GENERAL INFORMATION:
 ; APPLICANT: Goulmy, Elia
 ; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
 ; FILE REFERENCE: 58994
 ; CURRENT APPLICATION NUMBER: US/09/269,250E
 ; CURRENT FILING DATE: 1999-05-21
 ; NUMBER OF SEQ ID NOS: 38
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 18
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
 US-09-269-250E-18

Query Match 82.2%; Score 37; DB 2; Length 9;
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QY 1 VLAHDDLLEA 9
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 DB 1 VLAHDDLLEA 9

RESULT 4
 US-09-489-760-5
 ; Sequence 5, Application US/09489760
 ; Patent No. 6878375
 ; GENERAL INFORMATION:
 ; APPLICANT: Rijksuniversiteit Te Leiden
 ; APPLICANT: Goulmy, Elia A.J.M
 ; APPLICANT: Hunt, Donald F
 ; APPLICANT: Hard, Victor H
 ; TITLE OF INVENTION: The HA-1 Antigen
 ; FILE REFERENCE: 2183-4285US
 ; CURRENT APPLICATION NUMBER: US/09/489,760
 ; CURRENT FILING DATE: 2000-01-21
 ; EARLIER APPLICATION NUMBER: PCT/NL98/00424
 ; EARLIER FILING DATE: 1998-07-23
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 5
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: KIAA0223 partial complementary DNA
 US-09-489-760-5

Query Match 82.2%; Score 37; DB 2; Length 9;
 Best Local Similarity 88.9%; Pred. No. 4.6e+05;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLAHDDLLEA 9
 |||||
 DB 1 VLAHDDLLEA 9

RESULT 5

US-09-269-250E-29

; Sequence 29, Application US/09269250E
 ; Patent No. 6830883
 ; GENERAL INFORMATION:
 ; APPLICANT: Goulmy, Elia
 ; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
 ; FILE REFERENCE: 58994
 ; CURRENT APPLICATION NUMBER: US/09/269,250E
 ; CURRENT FILING DATE: 1999-05-21
 ; NUMBER OF SEQ ID NOS: 38
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 29
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: MISC FEATURE
 ; LOCATION: (3)..(3)
 ; OTHER INFORMATION: Xaa represents a histidine (H) or an arginine (R) residue
 US-09-269-250E-29

Query Match 80.0%; Score 36; DB 2; Length 9;
 Best Local Similarity 88.9%; Pred. No. 4.6e+05;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLAHDDLLEA 9
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 DB 1 VLAHDDLLEA 9

RESULT 6
 US-09-489-760-1
 ; Sequence 1, Application US/09489760
 ; Patent No. 6878375
 ; GENERAL INFORMATION:
 ; APPLICANT: Rijksuniversiteit Te Leiden
 ; APPLICANT: Goulmy, Elia A.J.M
 ; APPLICANT: Hunt, Donald F
 ; APPLICANT: Hard, Victor H
 ; TITLE OF INVENTION: The HA-1 Antigen
 ; FILE REFERENCE: 2183-4285US
 ; CURRENT APPLICATION NUMBER: US/09/489,760
 ; CURRENT FILING DATE: 2000-01-21
 ; EARLIER APPLICATION NUMBER: PCT/NL98/00424
 ; EARLIER FILING DATE: 1998-07-23
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Histocompatibility antigen
 ; FEATURE:
 ; NAME/KEY: PEPTIDE
 ; LOCATION: (3)
 ; OTHER INFORMATION: AMINO ACID X REPRESENTS A HISTIDINE OR AN ARGinine
 ; OTHER INFORMATION: RESIDUE
 US-09-489-760-1

Query Match 80.0%; Score 36; DB 2; Length 9;
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 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLAHDDLLEA 9
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 DB 1 VLAHDDLLEA 9

RESULT 7
 US-09-489-760-4
 ; Sequence 4, Application US/09489760
 ; Patent No. 6878375
 ; GENERAL INFORMATION:
 ; APPLICANT: Rijksuniversiteit Te Leiden

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 2, 2006, 21:46:48 ; Search time 42 Seconds
(without alignments)
89.535 Million cell updates/sec

Title: US-10-623-176a-2

Perfect score: 45

Sequence: 1 VLHDDLRA 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 180914

Minimum DB seq length: 0
Maximum DB seq length: 99

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	45	100.0	9	US-10-791-217-2	Sequence 2, Appli
3	45	100.0	9	US-10-861-335-1	Sequence 1, Appli
4	45	100.0	9	US-11-007-740-20	Sequence 20, Appli
5	41	91.1	9	US-10-623-176-41	Sequence 1, Appli
6	41	91.1	9	US-10-623-176-45	Sequence 45, Appli
7	37	82.2	9	US-10-623-176-10	Sequence 10, Appli
8	37	82.2	9	US-10-623-176-47	Sequence 47, Appli
9	37	82.2	9	US-10-791-217-5	Sequence 5, Appli
10	37	82.2	9	US-11-007-740-18	Sequence 18, Appli
11	36	80.0	9	US-10-623-176-1	Sequence 1, Appli
12	36	80.0	9	US-10-623-176-40	Sequence 40, Appli
13	36	80.0	9	US-10-791-217-1	Sequence 1, Appli
14	36	80.0	9	US-11-007-740-29	Sequence 29, Appli
15	33	73.3	9	US-10-623-176-42	Sequence 42, Appli
16	33	73.3	9	US-10-623-176-46	Sequence 46, Appli
17	33	73.3	9	US-10-623-176-4	Sequence 4, Appli
18	30	66.7	9	US-10-623-176-14	Sequence 14, Appli
19	30	66.7	9	US-11-007-740-4	Sequence 4, Appli
20	30	66.7	9	US-10-623-176-40	Sequence 40, Appli
21	29	63.4	9	US-10-623-176-48	Sequence 48, Appli
22	28.5	63.3	8	US-10-623-176-15	Sequence 15, Appli
23	28.5	63.3	8	US-11-007-740-38	Sequence 38, Appli
24	28	62.2	9	US-10-623-176-23	Sequence 23, Appli
25	28	62.2	9	US-10-623-176-38	Sequence 38, Appli
26	28	62.2	9	US-10-777-053-95	Sequence 95, Appli
27	28	62.2	9	US-10-837-217-95	Sequence 95, Appli

28	27	60.0	9	US-10-705-459-280	Sequence 280, App
29	26	57.8	6	US-10-166-225A-163	Sequence 163, App
30	26	57.8	6	US-10-166-225A-164	Sequence 164, App
31	26	57.8	6	US-10-166-225A-165	Sequence 165, App
32	26	57.8	6	US-10-166-225A-166	Sequence 166, App
33	26	57.8	6	US-10-166-225A-167	Sequence 167, App
34	25	55.6	6	US-10-166-225A-161	Sequence 161, App
35	25	55.6	6	US-10-166-225A-162	Sequence 162, App
36	25	55.6	7	US-09-803-951-5	Sequence 5, Appli
37	25	55.6	9	US-09-747-774A-3	Sequence 3, Appli
38	25	55.6	9	US-09-953-354-3	Sequence 3, Appli
39	25	55.6	9	US-10-267-074-14	Sequence 14, Appli
40	25	55.6	9	US-10-267-074-16	Sequence 16, Appli
41	25	55.6	9	US-10-752-478-3	Sequence 3, Appli
42	25	55.6	9	US-10-967-087-4	Sequence 4, Appli
43	24	53.3	7	US-10-020-354-86	Sequence 86, Appli
44	24	53.3	8	US-10-808-187-462	Sequence 462, App
45	24	53.3	8	US-10-807-807-462	Sequence 462, App

ALIGNMENTS

RESULT 1
US-10-623-176-2
Sequence 2, Application US/10623176
Publication No. US20040092446A1
GENERAL INFORMATION:
APPLICANT: Goulmy, Elie A.J.M.
APPLICANT: Hunt, Donald F.
TITLE OF INVENTION: HA-1 epitopes and uses thereof
FILE REFERENCE: 2183-60470S
CURRENT APPLICATION NUMBER: US/10/623,176
PRIOR FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/489,760
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: EP 97202303.0
PRIOR FILING DATE: 1997-07-23
PRIOR APPLICATION NUMBER: PCT/NL98/00424
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: JP 2000-504165
PRIOR FILING DATE: 2000-01-24
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide.
NAME/KEY: SITE
LOCATION: (1)..
US-10-623-176-2
Query Match
Best Local Similarity 100.0%; Score 45; DB 4; Length 9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 VLHDDLRA 9
DB 1 VLHDDLRA 9
RESULT 2
US-10-791-217-2
Sequence 2, Application US/10791217
Publication No. US20040191268A1
GENERAL INFORMATION:
APPLICANT: Goulmy, Elie A.J.M.
APPLICANT: Hunt, Donald F.
APPLICANT: Engelhard, Victor H


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;; TITLE OF INVENTION: The HA-1 Antigen
;; FILE REFERENCE: 2183-4285US
;; CURRENT APPLICATION NUMBER: US/10/791,217
;; CURRENT FILING DATE: 2004-03-02
;; PRIOR APPLICATION NUMBER: US/09/489,760
;; PRIOR FILING DATE: 2000-01-21
;; PRIOR APPLICATION NUMBER: PCT/NL98/00424
;; PRIOR FILING DATE: 1998-07-23
;; NUMBER OF SEQ ID NOS: 17
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 2
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; OTHER INFORMATION: obtained from histocompatibility antigen
US-10-791-217-2
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Query Match          100.0%; Score 45; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 VLAHDLLER 9
Db 1 VLAHDLLER 9
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RESULT 3
US-10-861-335-1
;; Sequence 1, Application US/10861335
;; Publication No. US20050031612A1
;; GENERAL INFORMATION:
;; APPLICANT: Goulmy, Elsa A.J.M.
;; TITLE OF INVENTION: Minor histocompatibility antigen HA-1: target antigen for immunot
;; FILE REFERENCE: 2183-6479US
;; CURRENT APPLICATION NUMBER: US/10/861,335
;; CURRENT FILING DATE: 2004-06-04
;; PRIOR APPLICATION NUMBER: PCT/NL02/00791
;; PRIOR FILING DATE: 2002-12-05
;; PRIOR APPLICATION NUMBER: EP 01204704.9
;; PRIOR FILING DATE: 2001-12-05
;; NUMBER OF SEQ ID NOS: 10
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 1
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: HA-1 peptide
US-10-861-335-1
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Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 VLAHDLLER 9
Db 1 VLAHDLLER 9
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RESULT 4
US-11-007-740-20
;; Sequence 20, Application US/11007740
;; Publication No. US2005023350A1
;; GENERAL INFORMATION:
;; APPLICANT: Goulmy, Elsa
;; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
;; FILE REFERENCE: 2799/58994-A
;; CURRENT APPLICATION NUMBER: US/11/007,740
;; CURRENT FILING DATE: 2004-12-08
;; PRIOR APPLICATION NUMBER: 09/269,250
;; PRIOR FILING DATE: 1999-05-21
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;; NUMBER OF SEQ ID NOS: 40
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 20
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-11-007-740-20
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Query Match          100.0%; Score 45; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 VLAHDLLER 9
Db 1 VLAHDLLER 9
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RESULT 5
US-10-623-176-41
;; Sequence 41, Application US/10623176
;; Publication No. US20040092446A1
;; GENERAL INFORMATION:
;; APPLICANT: Goulmy, Elsa A.J.M.
;; APPLICANT: Hunt, Donald F.
;; TITLE OF INVENTION: HA-1 epitopes and uses thereof
;; FILE REFERENCE: 2183-6047US
;; CURRENT APPLICATION NUMBER: US/10/623,176
;; CURRENT FILING DATE: 2003-07-18
;; PRIOR APPLICATION NUMBER: 09/489,760
;; PRIOR FILING DATE: 2000-01-21
;; PRIOR APPLICATION NUMBER: EP 97202303.0
;; PRIOR FILING DATE: 1997-07-23
;; PRIOR APPLICATION NUMBER: PCT/NL98/00424
;; PRIOR FILING DATE: 1998-07-23
;; PRIOR APPLICATION NUMBER: JP 2000-504165
;; PRIOR FILING DATE: 2000-01-24
;; NUMBER OF SEQ ID NOS: 77
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 41
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;; NAME/KEY: SITE
;; LOCATION: (1)..(9)
US-10-623-176-41
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Query Match          91.1%; Score 41; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 VLAHDLLER 8
Db 2 VLAHDLLER 9
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RESULT 6
US-10-623-176-45
;; Sequence 45, Application US/10623176
;; Publication No. US20040092446A1
;; GENERAL INFORMATION:
;; APPLICANT: Goulmy, Elsa A.J.M.
;; APPLICANT: Hunt, Donald F.
;; TITLE OF INVENTION: HA-1 epitopes and uses thereof
;; FILE REFERENCE: 2183-6047US
;; CURRENT APPLICATION NUMBER: US/10/623,176
;; CURRENT FILING DATE: 2003-07-18
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 2, 2006, 21:47:13 ; Search time 10 seconds
(without alignments)
18.000 Million cell updates/sec

Title: US-10-623-176a-2

Perfect score: 45

Sequence: 1 VHDDLLEA 9

Scoring table: BLOSUM62

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Searched: 135339 seqs, 20000136 residues 35206

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

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3: /cgn2_6/prodata/2/pubppa/US07_NEW_PUB.pep.*
4: /cgn2_6/prodata/2/pubppa/PCT_NEW_PUB.pep.*
5: /cgn2_6/prodata/2/pubppa/US09_NEW_PUB.pep.*
6: /cgn2_6/prodata/2/pubppa/US10_NEW_PUB.pep.*
7: /cgn2_6/prodata/2/pubppa/US11_NEW_PUB.pep.*
8: /cgn2_6/prodata/2/pubppa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	37	82.2	9	7	US-11-010-748A-12
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4	26	57.8	6	7	US-11-129-143-164
5	26	57.8	6	7	US-11-129-143-165
6	26	57.8	6	7	US-11-129-143-166
7	25	55.6	6	7	US-11-129-143-161
8	25	55.6	6	7	US-11-129-143-162
9	23	51.1	6	6	US-10-485-788A-353
10	23	51.1	6	6	US-10-485-788A-354
11	23	51.1	8	6	US-10-485-788A-355
12	23	51.1	7	7	US-11-033-039-785
13	23	51.1	9	7	US-11-033-039-809
14	22	48.9	5	6	US-10-485-788A-352
15	22	48.9	6	6	US-10-857-435A-443
16	22	48.9	7	6	US-10-857-435A-444
17	22	48.9	8	7	US-11-045-024-444
18	22	48.9	8	7	US-11-045-024-445
19	22	48.9	8	7	US-11-045-024-7094
20	22	48.9	9	7	US-11-045-024-607
21	22	48.9	9	7	US-11-045-024-3715
22	22	48.9	9	7	US-11-045-024-5511
23	22	48.9	9	7	US-11-045-024-12585
24	22	48.9	9	7	US-11-045-024-14029
25	21	46.7	4	6	US-10-485-788A-351

26	20	44.4	4	6	US-10-667-295-263	Sequence 263, App
27	20	44.4	4	6	US-10-857-435A-366	Sequence 366, App
28	20	44.4	4	7	US-11-019-027-5	Sequence 5, Appl1
29	20	44.4	4	7	US-11-174-413-64	Sequence 64, Appl1
30	20	44.4	4	7	US-11-108-088-69	Sequence 69, Appl1
31	20	44.4	5	7	US-11-129-143-168	Sequence 168, App
32	20	44.4	5	7	US-11-129-143-169	Sequence 169, App
33	20	44.4	5	7	US-11-129-143-170	Sequence 170, App
34	20	44.4	5	7	US-11-129-143-171	Sequence 171, App
35	20	44.4	5	7	US-11-129-143-172	Sequence 172, App
36	20	44.4	5	7	US-10-857-435A-367	Sequence 367, App
37	20	44.4	6	6	US-10-857-435A-367	Sequence 397, App
38	20	44.4	6	6	US-10-857-435A-367	Sequence 667, App
39	20	44.4	6	7	US-11-021-305-62	Sequence 62, Appl1
40	20	44.4	8	7	US-11-021-305-65	Sequence 65, Appl1
41	20	44.4	8	7	US-11-021-305-66	Sequence 66, Appl1
42	20	44.4	9	6	US-10-522-912-5	Sequence 5, Appl1
43	20	44.4	9	6	US-10-522-912-8	Sequence 8, Appl1
44	20	44.4	9	6	US-10-510-101-62	Sequence 62, Appl1

ALIGNMENTS

RESULT 1
US-11-010-748A-11
Sequence 11, Application US/11010748A
Publication No. US20050244421A1
GENERAL INFORMATION:
APPLICANT: Merck Patent GmbH
APPLICANT: STRITTMAYER, Wolfgang
APPLICANT: MOUL, Heidrun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
FILE REFERENCE: MER-136
CURRENT APPLICATION NUMBER: US/11/010,748A
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/EP03/06251
PRIOR FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: EP02013423.5
PRIOR FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 926
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: NAME/KEY: MISC_FEATURE
LOCATION: (1)..(9)
OTHER INFORMATION: Human minor histocompatibility antigens HA-1 characterized by T c
US-11-010-748A-11

Query Match 100.0%; Score 45; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHDDLLEA 9
DB 1 VHDDLLEA 9

RESULT 2
US-11-010-748A-12
Sequence 12, Application US/11010748A
Publication No. US20050244421A1
GENERAL INFORMATION:
APPLICANT: Merck Patent GmbH
APPLICANT: STRITTMAYER, Wolfgang
APPLICANT: MOUL, Heidrun
APPLICANT: SCHAM, Burkhard


```

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(9)
; OTHER INFORMATION: Human minor histocompatibility antigens HA-1 characterized by T C
; OTHER INFORMATION: all epitopes
US-11-010-748A-12

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Query Match      82.2%; Score 37; DB 7; Length 9;
Best Local Similarity 88.9%; Pred. No. 1e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 11111111
DB      1 VLHDDLLEA 9

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RESULT 3
US-11-129-143-163
; Sequence 163, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 163
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
US-11-129-143-163

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Query Match      57.8%; Score 26; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 1e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

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QY      2 111111
DB      1 IHDDL 5

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RESULT 4
US-11-129-143-164
; Sequence 164, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.

```

```

; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 164
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-11-129-143-164

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Query Match      57.8%; Score 26; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 1e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 111111
DB      1 IHDDL 5

```

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RESULT 5
US-11-129-143-165
; Sequence 165, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 165
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Escherichia coli
US-11-129-143-165

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```

Query Match      57.8%; Score 26; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 1e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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```

QY      2 111111
DB      1 IHDDL 5

```

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RESULT 6
US-11-129-143-166
; Sequence 166, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 166
; LENGTH: 6
; TYPE: PRT

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